

[illegible]

(i) APPLICANTS: RICHARD MARTIN BROGLIE
LORIN ROGER DE BONTE
WILLIAM DEAN HITZ
GUO-HUA MIAO
ROBERT STEFAN REITER

(ii) TITLE OF INVENTION: GENES FOR MUTANT MICROSOMAL
FATTY ACID DELTA-12
DESATURASES AND RELATED
ENZYMES FROM PLANTS

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
(B) STREET: 1007 MARKET STREET
(C) CITY: WILMINGTON
(D) STATE: DELAWARE
(E) COUNTRY: U.S.A.
(F) ZIP: 19898

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
(D) SOFTWARE: MICROSOFT OFFICE 97

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/232,948
(B) FILING DATE: January 19, 1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/256,047
(B) FILING DATE: NOVEMBER 17, 1992

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lynne M. Christenbury
(C) REFERENCE/DOCKET NUMBER: BB-1334-A

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (302) 992-5481
(B) TELEFAX: (302) 892-7949
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1464 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 130..1281
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGCACGAGCT CGTGCCGAAT TCGGCACGAG AGGAGACAGA GAGAGAGTTT GAGGAGGAGC      60
TTCTTCGTAG GGTTCATCGT TATTAACGTT AAATCTTCAT CCCCCCTAC GTCAGCCAGC      120
TCAAGAAAC ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC      168
      Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser
        1                      5                      10

AAA AAG TCT GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG      216
Lys Lys Ser Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro
      15                      20                      25

CCC TTC ACT GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC      264
Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe
      30                      35                      40                      45

AAA CGC TCG ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC      312
Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile
                      50                      55                      60

ATA GCC TCC TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC      360
Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu
                      65                      70                      75

CCT CAC CCT CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG      408
Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln
                      80                      85                      90

GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC      456
Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His
      95                      100                      105

CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC      504
His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile
      110                      115                      120                      125

TTC CAC TCC TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT      552
Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His
                      130                      135                      140

CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT      600
Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe
                      145                      150                      155

GTC CCC AAG AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC      648
Val Pro Lys Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn
      160                      165                      170

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AAC CCT TTG GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC	696
Asn Pro Leu Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly	
175 180 185	
TGG CCT TTG TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC	744
Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly	
190 195 200 205	
GGC TTC GCT TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGT	792
Gly Phe Ala Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg	
210 215 220	
GAG CGT CTC CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC	840
Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys	
225 230 235	
TAC GGT CTC TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC	888
Tyr Gly Leu Tyr Arg Tyr Ala Val Gln Gly Val Ala Ser Met Val	
240 245 250	
TGC TTC TAC GGA GTT CCT CTT CTG ATT GTC AAC GGG TTC TTA GTT TTG	936
Cys Phe Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu	
255 260 265	
ATC ACT TAC TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG	984
Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser	
270 275 280 285	
TCT GAG TGG GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC	1032
Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp	
290 295 300	
TAC GGA ATC TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG	1080
Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val	
305 310 315	
GCG CAT CAC CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT	1128
Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala	
320 325 330	
ACG AAG GCG ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG	1176
Thr Lys Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly	
335 340 345	
ACG CCG GTG GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT	1224
Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr	
350 355 360 365	
GTG GAA CCG GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC	1272
Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn	
370 375 380	
AAT AAG TTA TGAAGCAAAG AAGAACTGA ACCTTTCTCT TCTATGATTG	1321
Asn Lys Leu	
TCTTTGTTTA AGAAGCTATG TTTCTGTTTC AATAATCTTA ATTATCCATT TTGTTGTGTT	1381
TTCTGACATT TTGGCTAAAA TTATGTGATG TTGGAAGTTA GTGTCTAAAA AAAAAAAAAA	1441
AAAAAAAAAA AAAAAAAAAA AAA	1464

275	280	285
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile		
290	295	300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His		
305	310	315
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala		
	325	330
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val		
	340	345
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro		
	355	360
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu		
370	375	380

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Brassica napus
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: IMC129
- (ix) FEATURE:
 - (D) OTHER INFORMATION: G to A transversion
mutation at nucleotide 316
of the D form
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT	48
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
1 5 10 15	
GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT	96
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	

CTC Leu	TCC Ser	TAC Tyr	TTC Phe	GCC Ala 85	TGG Trp	CCT Pro	CTC Leu	TAC Tyr	TGG Trp 90	GCC Ala	TGC Cys	CAG Gln	GGC Gly	TGC Cys 95	GTC Val	288
CTA Leu	ACC Thr	GGC Gly	GTC Val 100	TGG Trp	GTC Val	ATA Ile	GCC Ala	CAC His 105	AAG Lys	TGC Cys	GGC Gly	CAC His 110	CAC His Ala	GCC Ala	TTC Phe	336
AGC Ser	GAC Asp	TAC Tyr 115	CAG Gln	TGG Trp	CTG Leu	GAC Asp	GAC Asp 120	ACC Thr	GTC Val	GGC Gly	CTC Leu	ATC Ile 125	TTC Phe	CAC His	TCC Ser	384
TTC Phe 130	CTC Leu	CTC Leu	GTC Val	CCT Pro	TAC Tyr	TTC Phe 135	TCC Ser	TGG Trp	AAG Lys	TAC Tyr	AGT Ser 140	CAT His	CGA Arg	CGC Arg	CAC His	432
CAT His 145	TCC Ser	AAC Asn	ACT Thr	GGC Gly	TCC Ser 150	CTC Leu	GAG Glu	AGA Arg	GAC Asp	GAA Glu 155	GTG Val	TTT Phe	GTC Val	CCC Pro	AAG Lys 160	480
AAG Lys	AAG Lys	TCA Ser	GAC Asp	ATC Ile 165	AAG Lys	TGG Trp	TAC Tyr	GGC Gly	AAG Lys 170	TAC Tyr	CTC Leu	AAC Asn	AAC Asn	CCT Pro 175	TTG Leu	528
GGA Gly	CGC Arg	ACC Thr	GTG Val 180	ATG Met	TTA Leu	ACG Thr	GTT Val	CAG Gln 185	TTC Phe	ACT Thr	CTC Leu	GGC Gly	TGG Trp 190	CCT Pro	TTG Leu	576
TAC Tyr	TTA Leu	GCC Ala 195	TTC Phe	AAC Asn	GTC Val	TCG Ser	GGG Gly 200	AGA Arg	CCT Pro	TAC Tyr	GAC Asp	GGC Gly 205	GGC Gly	TTC Phe	GCT Ala	624
TGC Cys 210	CAT His	TTC Phe	CAC His	CCC Pro	AAC Asn	GCT Ala 215	CCC Pro	ATC Ile	TAC Tyr	AAC Asn	GAC Asp 220	CGC Arg	GAG Glu	CGT Arg	CTC Leu	672
CAG Gln 225	ATA Ile	TAC Tyr	ATC Ile	TCC Ser	GAC Asp 230	GCT Ala	GGC Gly	ATC Ile	CTC Leu	GCC Ala 235	GTC Val	TGC Cys	TAC Tyr	GGT Gly	CTC Leu 240	720
TAC Tyr	CGC Arg	TAC Tyr	GCT Ala	GCT Ala 245	GTC Val	CAA Gln	GGA Gly	GTT Val	GCC Ala 250	TCG Ser	ATG Met	GTC Val	TGC Cys	TTC Phe 255	TAC Tyr	768
GGA Gly	GTT Val	CCG Pro	CTT Leu 260	CTG Leu	ATT Ile	GTC Val	AAT Asn	GGG Gly 265	TTC Phe	TTA Leu	GTT Val	TTG Leu 270	ATC Ile	ACT Thr	TAC Tyr	816
TTG Leu	CAG Gln	CAC His 275	ACG Thr	CAT His	CCT Pro	TCC Ser	CTG Leu 280	CCT Pro	CAC His	TAT Tyr	GAC Asp 285	TCG Ser	TCT Ser	GAG Glu	TGG Trp	864
GAT Asp	TGG Trp 290	TTG Leu	AGG Arg	GGA Gly	GCT Ala	TTG Leu 295	GCC Ala	ACC Thr	GTT Val	GAC Asp	AGA Arg 300	GAC Asp	TAC Tyr	GGA Gly	ATC Ile	912
TTG Leu 305	AAC Asn	AAG Lys	GTC Val	TTC Phe	CAC His 310	AAT Asn	ATC Ile	ACG Thr	GAC Asp	ACG Thr 315	CAC His	GTG Val	GCG Ala	CAT His	CAC His 320	960

CTG	TTC	TCG	ACC	ATG	CCG	CAT	TAT	CAT	GCG	ATG	GAA	GCT	ACG	AAG	GCG	1008
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala	
				325					330					335		
ATA	AAG	CCG	ATA	CTG	GGA	GAG	TAT	TAT	CAG	TTC	GAT	GGG	ACG	CCG	GTG	1056
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val	
			340					345					350			
GTT	AAG	GCG	ATG	TGG	AGG	GAG	GCG	AAG	GAG	TGT	ATC	TAT	GTG	GAA	CCG	1104
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	
		355					360					365				
GAC	AGG	CAA	GGT	GAG	AAG	AAA	GGT	GTG	TTC	TGG	TAC	AAC	AAT	AAG	TTA	T 1153
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu	
	370					375					380					
GA																1155

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Ala	Gly	Gly	Arg	Met	Gln	Val	Ser	Pro	Pro	Ser	Lys	Lys	Ser	
1				5					10					15		
Glu	Thr	Asp	Asn	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr	
			20					25					30			
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	
		35					40					45				
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser	
	50					55					60					
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro	
65					70					75					80	
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	
				85					90					95		
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Lys	Cys	Gly	His	His	Ala	Phe	
			100					105					110			
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	
	115					120						125				
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	
	130					135					140					
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	
145					150					155					160	
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	
				165					170					175		

002260 02521960

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Brassica napus
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Wild type F form.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT
 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser

1	5				10				15								
GAA Glu	ACC Thr	GAC Asp	ACC Thr 20	ATC Ile	AAG Lys	CGC Arg	GTA Val	CCC Pro 25	TGC Cys	GAG Glu	ACA Thr	CCG Pro	CCC Pro 30	TTC Phe	ACT Thr		96
GTC Val	GGA Gly	GAA Glu 35	CTC Leu	AAG Lys	AAA Lys	GCA Ala	ATC Ile 40	CCA Pro	CCG Pro	CAC His	TGT Cys	TTC Phe 45	AAA Lys	CGC Arg	TCG Ser		144
ATC Ile	CCT Pro 50	CGC Arg	TCT Ser	TTC Phe	TCC Ser	TAC Tyr 55	CTC Leu	ATC Ile	TGG Trp	GAC Asp 60	ATC Ile	ATC Ile	ATA Ile	GCC Ala	TCC Ser		192
TGC Cys 65	TTC Phe	TAC Tyr	TAC Tyr	GTC Val	GCC Ala 70	ACC Thr	ACT Thr	TAC Tyr	TTC Phe	CCT Pro 75	CTC Leu	CTC Leu	CCT Pro	CAC His	CCT Pro 80		240
CTC Leu	TCC Ser	TAC Tyr	TTC Phe	GCC Ala 85	TGG Trp	CCT Pro	CTC Leu	TAC Tyr	TGG Trp 90	GCC Ala	TGC Cys	CAA Gln	GGG Gly	TGC Cys 95	GTC Val		288
CTA Leu	ACC Thr	GGC Gly	GTC Val 100	TGG Trp	GTC Val	ATA Ile	GCC Ala 105	CAC His	GAG Glu	TGC Cys	GGC Gly	CAC His 110	CAC His	GCC Ala	TTC Phe		336
AGC Ser	GAC Asp	TAC Tyr 115	CAG Gln	TGG Trp	CTT Leu	GAC Asp 120	GAC Asp	ACC Thr	GTC Val	GGT Gly	CTC Leu	ATC Ile 125	TTC Phe	CAC His	TCC Ser		384
TTC Phe 130	CTC Leu	CTC Leu	GTC Val	CCT Pro	TAC Tyr	TTC Phe 135	TCC Ser	TGG Trp	AAG Lys	TAC Tyr	AGT Ser 140	CAT His	CGC Arg	AGC Ser	CAC His		432
CAT His 145	TCC Ser	AAC Asn	ACT Thr	GGC Gly	TCC Ser 150	CTC Leu	GAG Glu	AGA Arg	GAC Asp	GAA Glu 155	GTG Val	TTT Phe	GTC Val	CCC Pro	AAG Lys 160		480
AAG Lys	AAG Lys	TCA Ser	GAC Asp 165	ATC Ile	AAG Lys	TGG Trp	TAC Tyr	GGC Gly	AAG Lys 170	TAC Tyr	CTC Leu	AAC Asn	AAC Asn	CCT Pro 175	TTG Leu		528
GGA Gly	CGC Arg	ACC Thr	GTG Val 180	ATG Met	TTA Leu	ACG Thr	GTT Val	CAG Gln 185	TTC Phe	ACT Thr	CTC Leu	GGC Gly	TGG Trp 190	CCG Pro	TTG Leu		576
TAC Tyr	TTA Leu	GCC Ala 195	TTC Phe	AAC Asn	GTC Val	TCG Ser	GGA Gly 200	AGA Arg	CCT Pro	TAC Tyr	GAC Asp	GGC Gly 205	GGC Gly	TTC Phe	CGT Arg		624
TGC Cys 210	CAT His	TTC Phe	CAC His	CCC Pro	AAC Asn	GCT Ala 215	CCC Pro	ATC Ile	TAC Tyr	AAC Asn	GAC Asp 220	CGC Arg	GAG Glu	CGT Arg	CTC Leu		672
CAG Gln 225	ATA Ile	TAC Tyr	ATC Ile	TCC Ser	GAC Asp 230	GCT Ala	GGC Gly	ATC Ile	CTC Leu	GCC Ala 235	GTC Val	TGC Cys	TAC Tyr	GGT Gly	CTC Leu 240		720
TTC Phe	CGT Arg	TAC Tyr	GCC Ala 245	GCC Ala	GGC Gly	CAG Gln	GGA Gly	GTG Val	GCC Ala 250	TCG Ser	ATG Met	GTC Val	TGC Cys	TTC Phe 255	TAC Tyr		768
GGA Gly	GTC Arg	CCG Thr	CTT Ser	CTG Val	ATT Leu	GTC Val	AAT Leu	GGT Val	TTC Val	CTC Val	GTG Val	TTG Val	ATC Val	ACT Val	TAC Val		816

Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr		
			260					265					270				
TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAC	GAT	TCG	TCC	GAG	TGG	864	
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp		
		275					280					285					
GAT	TGG	TTC	AGG	GGA	GCT	TTG	GCT	ACC	GTT	GAC	AGA	GAC	TAC	GGA	ATC	912	
Asp	Trp	Phe	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile		
	290					295					300						
TTG	AAC	AAG	GTC	TTC	CAC	AAT	ATT	ACC	GAC	ACG	CAC	GTG	GCC	CAT	CAT	960	
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His		
305					310					315					320		
CCG	TTC	TCC	ACG	ATG	CCG	CAT	TAT	CAC	GCG	ATG	GAA	GCT	ACC	AAG	GCG	1008	
Pro	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala		
				325					330					335			
ATA	AAG	CCG	ATA	CTG	GGA	GAG	TAT	TAT	CAG	TTC	GAT	GGG	ACG	CCG	GTG	1056	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val		
			340					345					350				
GTT	AAG	GCG	ATG	TGG	AGG	GAG	GCG	AAG	GAG	TGT	ATC	TAT	GTG	GAA	CCG	1104	
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro		
		355					360					365					
GAC	AGG	CAA	GGT	GAG	AAG	AAA	GGT	GTG	TTC	TGG	TAC	AAC	AAT	AAG	TTA	T	1153
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu		
	370					375					380						
GA																	1155

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Ala	Gly	Gly	Arg	Met	Gln	Val	Ser	Pro	Pro	Ser	Lys	Lys	Ser
1				5					10					15	
Glu	Thr	Asp	Thr	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr
			20					25					30		
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
		35					40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser
	50					55					60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro
65					70					75					80
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
				85					90					95	
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe

100					105					110					
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
		115					120					125			
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His
	130					135					140				
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
				165					170					175	
Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu
			180					185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg
		195					200					205			
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu
	210					215					220				
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
			245						250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
		275					280					285			
Asp	Trp	Phe	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290				295					300					
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Pro	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
				325					330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val
			340					345					350		
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
		355					360					365			
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu
	370				375					380					

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Brassica napus

(vii) IMMEDIATE SOURCE:
(B) CLONE: IMC Q508

(ix) FEATURE:
(D) OTHER INFORMATION: T to A transversion
mutation at nucleotide 515
of the F form

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT	48
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
1 5 10 15	
GAA ACC GAC AGC ATC AAG CGC GTA GCC TGC GAG ACA CGG GCC TTC ACT	96
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC CAC GCC TTC	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His	
130 135 140	
CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CAC AAC AAC CCT TTG	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu	
165 170 175	
GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	

	180							185							190							
TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGA	AGA	CCT	TAC	GAC	GGC	GGC	TTC	CGT	624						
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg							
		195					200					205										
TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC	672						
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu							
	210					215					220											
CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC	720						
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu							
225					230					235					240							
TTC	CGT	TAC	GCC	GCC	GGC	CAG	GGA	GTG	GCC	TCG	ATG	GTC	TGC	TTC	TAC	768						
Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr							
				245					250					255								
GGA	GTC	CCG	CTT	CTG	ATT	GTC	AAT	GGT	TTC	CTC	GTG	TTG	ATC	ACT	TAC	816						
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr							
			260					265					270									
TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAC	GAT	TCG	TCC	GAG	TGG	864						
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp							
		275					280					285										
GAT	TGG	TTC	AGG	GGA	GCT	TTG	GCT	ACC	GTT	GAC	AGA	GAC	TAC	GGA	ATC	912						
Asp	Trp	Phe	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile							
	290					295					300											
TTG	AAC	AAG	GTC	TTC	CAC	AAT	ATT	ACC	GAC	ACG	CAC	GTG	GCC	CAT	CAT	960						
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His							
305					310					315					320							
CCG	TTC	TCC	ACG	ATG	CCG	CAT	TAT	CAC	GCG	ATG	GAA	GCT	ACC	AAG	GCG	1008						
Pro	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala							
				325					330					335								
ATA	AAG	CCG	ATA	CTG	GGA	GAG	TAT	TAT	CAG	TTC	GAT	GGG	ACG	CCG	GTG	1056						
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val							
			340					345					350									
GTT	AAG	GCG	ATG	TGG	AGG	GAG	GCG	AAG	GAG	TGT	ATC	TAT	GTG	GAA	CCG	1104						
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro							
		355					360					365										
GAC	AGG	CAA	GGT	GAG	AAG	AAA	GGT	GTG	TTC	TGG	TAC	AAC	AAT	AAG	TTA	1153						
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu							
	370					375					380											
GA																1155						

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gly	Ala	Gly	Gly	Arg	Met	Gln	Val	Ser	Pro	Pro	Ser	Lys	Lys	Ser
1				5					10					15	
Glu	Thr	Asp	Thr	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr
			20					25					30		
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
		35					40					45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser
	50					55					60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro
65					70					75					80
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
				85					90					95	
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
			100					105					110		
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
		115					120					125			
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His
	130					135					140				
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	His	Asn	Asn	Pro	Leu
				165					170					175	
Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu
			180					185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg
		195					200					205			
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu
	210					215					220				
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
			245						250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
		275					280					285			
Asp	Trp	Phe	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Pro	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
				325					330					335	

Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATGGGTGCA GGTGGAAGAA TGC

23

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTTTCTTCTT TGCTTCATAA C

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGGGTGCA GGTGGAAGAA TGC

23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCTTTCACCA TCATCATATC C

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCTGGGTCA TAGCCCACG

19

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTCTGGGTCA TAGCCCACA

19

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGGGTCATA GCCCATG

17

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGGGTCATA GCCCACA

17

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /product= "Asp or Glu"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "Ala or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Xaa Cys Xaa His
1 5